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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/907,007

DATE: 08/08/2001  
 TIME: 19:26:16

Input Set : N:\Crf3\RULE60\09907007.txt  
 Output Set: N:\CRF3\08082001\I907007.raw

C--> 4 <110> APPLICANT: Hayward, Nicholas K.  
 5 Weber, Gunther  
 6 Grimmond, Sean  
 7 Nordenskjold, Magnus  
 8 Larsson, Catharina  
 10 <120> TITLE OF INVENTION: A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING  
 11 SAME  
 13 <130> FILE REFERENCE: DAVIES  
 15 <140> CURRENT APPLICATION NUMBER: 09/907,007  
 16 <141> CURRENT FILING DATE: 2001-07-17  
 18 <150> PRIOR APPLICATION NUMBER: 08/765,588  
 19 <151> PRIOR FILING DATE: 1996-02-22  
 21 <160> NUMBER OF SEQ ID NOS: 22  
 23 <170> SOFTWARE: PatentIn Ver. 2.1  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 649  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Nucleotide Sequence of VEGF165  
 30 <220> FEATURE:  
 31 <221> NAME/KEY: CDS  
 32 <222> LOCATION: (17)..(589)  
 34 <400> SEQUENCE: 1  
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 38 1 5 10  
 40 gcc ttg ctg ctc tac ctc cac cat gcc aag tgg tcc cag gct gca ccc 100  
 42 Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro  
 43 15 20 25  
 45 atg gca gaa gga gga ggg cag aat cat cac gaa gtg gtg aag ttc atg 148  
 47 Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met  
 48 30 35 40  
 50 gat gtc tat cag cgc agc tac tgc cat cca atc gag acc ctg gtg gac 196  
 52 Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp  
 53 45 50 55 60  
 55 atc ttc cag gag tac cct gat gag atc gag tac atc ttc aag cca tcc 244  
 57 Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser  
 58 65 70 75  
 60 tgt gtg ccc ctg atg cga tgc ggg ggc tgc tgc aat gac gag ggc ctg 292  
 62 Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu  
 63 80 85 90  
 65 gag tgt gtg ccc act gag gag tcc aac atc acc atg cag att atg cgg 340  
 67 Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg  
 68 95 100 105  
 70 atc aaa cct cac caa ggc cag cac ata gga gag atg agc ttc cta cag 388  
 72 Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln  
 73 110 115 120  
 75 cac aac aaa tgt gaa tgc aga cca aag aaa gat aga gca aga caa gaa 436

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78 125                               130                               135                               140
80 aat ccc tgt ggg cct tgc tca gag cgg aga aag cat ttg ttt gta caa 484
82 Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln
83                               145                               150                               155
85 gat ccg cag acg tgt aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc 532
87 Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys
88                               160                               165                               170
90 aag gcg agg cag ctt gag tta aac gaa cgt act tgc aga tgt gac aag 580
92 Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys
93                               175                               180                               185
95 ccg agg cgg tgagccgggc aggaggaagg agcctccctc agcgtttcgg 629
97 Pro Arg Arg
98 190
100 gaaccagatc tctcaccagg 649
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106 <212> TYPE: PRT
107 <213> ORGANISM: Nucleotide Sequence of VEGF165
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113 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
114 20 25 30
116 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
117 35 40 45
119 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
120 50 55 60
122 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
123 65 70 75 80
125 Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
126 85 90 95
128 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
129 100 105 110
131 Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
132 115 120 125
134 Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
135 130 135 140
137 Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
138 145 150 155 160
140 Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
141 165 170 175
143 Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
144 180 185 190
148 <210> SEQ ID NO: 3
149 <211> LENGTH: 1094
150 <212> TYPE: DNA
151 <213> ORGANISM: Nucleotide Sequence of SOM175
153 <220> FEATURE:

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161 1 5 10 15
163 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95
165 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
166 20 25 30
168 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143
170 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
171 35 40 45
173 cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191
175 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
176 50 55 60
178 gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239
180 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
181 65 70 75
183 ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287
185 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
186 80 85 90 95
188 caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg 335
190 Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
191 100 105 110
193 ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa 383
195 Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
196 115 120 125
198 aaa aag gac agt gct gtg aag cca gac agg gct gcc act ccc cac cac 431
200 Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His
201 130 135 140
203 cgt ccc cag ccc cgt tct gtt ccg ggc tgg gac tct gcc ccc gga gca 479
205 Arg Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala
206 145 150 155
208 ccc tcc cca gct gac atc acc cat ccc act cca gcc cca ggc ccc tct 527
210 Pro Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser
211 160 165 170 175
213 gcc cac gct gca ccc agc acc acc agc gcc ctg acc ccc gga cct gcc 575
215 Ala His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala
216 180 185 190
218 gct gcc gct gcc gac gcc gca gct tcc tcc gtt gcc aag ggc ggg gct 623
220 Ala Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
221 195 200 205
223 tagagctcaa ccagacacc tgcaggtgcc ggaagctgcg aaggtgacac atggcttttc 683
226 agactcagca ggggtgacttg cctcagaggc tatatcccag tgggggaaca aaggggagcc 743
229 tggtaaaaaa cagccaagcc cccaagacct cagcccaggc agaagctgct ctaggacctg 803
232 ggcctctcag agggtctctt tgcctccctt tgtctccctg aggccatcat caaacaggac 863
235 agagttggaa gaggagactg ggaggcagca agaggggtca cataccagct caggggagaa 923
238 tggagtactg tctcagtttc taaccactct gtgcaagtaa gcatcttaca actggctctt 983
241 cctcccctca ctaagaagac ccaaacctct gcataatggg atttgggctt tgggtacaaga 1043

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 249 <211> LENGTH: 207  
 250 <212> TYPE: PRT  
 251 <213> ORGANISM: Nucleotide Sequence of SOM175  
 253 <400> SEQUENCE: 4  
 254 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu  
 255 1 5 10 15  
 257 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln  
 258 20 25 30  
 260 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln  
 261 35 40 45  
 263 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val  
 264 50 55 60  
 266 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly  
 267 65 70 75 80  
 269 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln  
 270 85 90 95  
 272 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly  
 273 100 105 110  
 275 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys  
 276 115 120 125  
 278 Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg  
 279 130 135 140  
 281 Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro  
 282 145 150 155 160  
 284 Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala  
 285 165 170 175  
 287 His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala  
 288 180 185 190  
 290 Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala  
 291 195 200 205  
 295 <210> SEQ ID NO: 5  
 296 <211> LENGTH: 993  
 297 <212> TYPE: DNA  
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 301 <221> NAME/KEY: CDS  
 302 <222> LOCATION: (3)..(566)  
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 308 1 5 10 15  
 310 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95  
 312 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His 30  
 313 20 25 30  
 315 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143  
 317 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys 45  
 318 35 40 45

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320 cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191
322 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
323          50          55          60
325 gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239
327 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
328          65          70          75
330 ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287
332 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
333 80          85          90          95
335 caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg 335
337 Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
338          100          105          110
340 ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa 383
342 Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
343          115          120          125
345 aaa aag gac agt gct gtg aag cca gat agc ccc agg ccc ctc tgc cca 431
347 Lys Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro
348          130          135          140
350 cgc tgc acc cag cac cac cag cgc cct gac ccc cgg acc tgc cgc tgc 479
352 Arg Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys
353          145          150          155
355 cgc tgc cga cgc cgc agc ttc ctc cgt tgc caa ggg cgg ggc tta gag 527
357 Arg Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu
358 160          165          170          175
360 ctc aac cca gac acc tgc agg tgc cgg aag ctg cga agg tgacacatgg 576
362 Leu Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
363          180          185
365 cttttcagac tcagcagggt gacttgcttc agaggctata tcccagtgagg ggaacaaagg 636
368 ggagcctggt aaaaaacagc caagcccccag agacctcagc ccaggcagaa gctgctctag 696
371 gacctgggccc tctcagagggt ctcttctgcc atcccttgct tccctgaggc catcatcaaa 756
374 caggacagag ttggaagagg agactgggag gcagcaagag gggtcacata ccagctcagg 816
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380 gctcttcttc ccctcactaa gaagacccaa acctctgcat aatgggattt gggctttggg 936
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388 <211> LENGTH: 188
389 <212> TYPE: PRT
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397          20          25          30
399 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
400          35          40          45
402 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
403          50          55          60
405 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
406 65          70          75          80

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**VERIFICATION SUMMARY**

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L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date